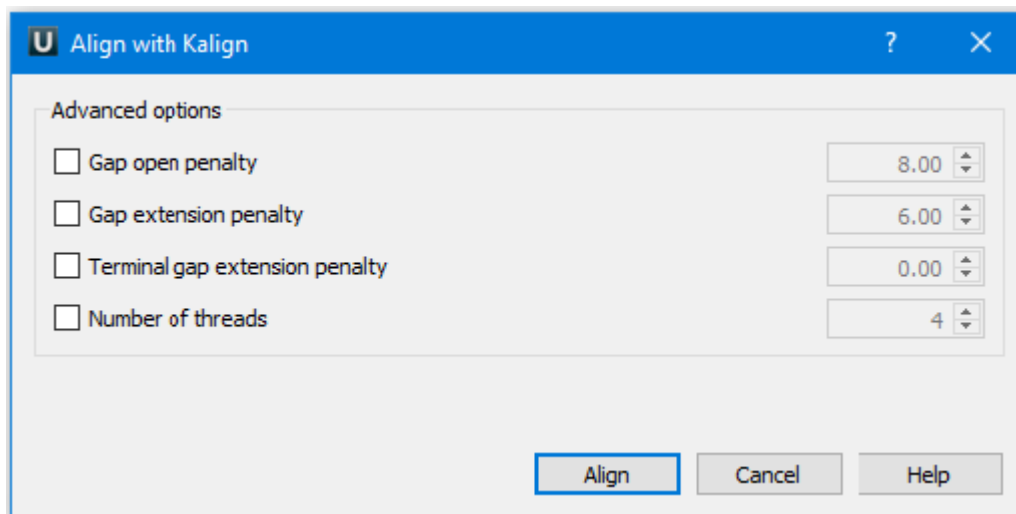# Kalign Aligning

Kalign is a fast and accurate multiple sequence package designed to align large numbers of protein sequences.

Kalign home page: KAlign

To use *Kalign* open a multiple sequence alignment file and select the *Align with Kalign* item in the context menu or in the *Actions* main menu. The following dialog appears:

The following parameters are available:

Gap opening penalty — indicates the penalty applied for opening a gap. The penalty must be negative.

Gap extension penalty — indicates the penalty applied for extending a gap.

Terminal gap penalty — the penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.

Number of thread — number of threads.

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